AMENDMENTS

In the Specification:

Please replace paragraph [0067] on page 17 with the following paragraph:

[0067] Figure 3 is a graphic representation illustrating that Dam regulates *in vivo* induced genes. β-galactosidase expression from *S. typhimurium ivi* fusions in Dam^+ and Dam^- strains grown in LB. The vertical axis shows β-galactosidase activities (μ-moles of o-nitrophenol (ONP) formed per minute per A_{600} unit per milliliter of cell suspension x 10^3).

Please replace paragraph [0068] on page 18 with the following paragraph:

[0068] Figure 4 is a graphic representation illustrating that Dam represses PhoP activated genes. β-galactosidase expression from *S. typhimurium ivi* fusions grown in minimal medium. The vertical axis shows β-galactosidase activities (μ-moles of o-nitrophenol (ONP) formed per minute per A_{600} unit per milliliter of cell suspension x 10^3). The *dam* genotype is shown below the horizontal axis, and the *phoP* genotype is shown as black ($PhoP^+$) and gray ($PhoP^-$) boxes.

Please replace paragraph [00244] on pages 67-68 with the following paragraph:

[00244] All bacterial strains used in this study were derivatives of *S. typhimurium* 14028 (strain **1**). Mutant strains were isogenic to wild type and were obtained or constructed as described (*Dam102*::Mu*d*-Cm and *mutS121*::Tn*10* alleles are in LT2 (strain **7**), a highly attenuated (virtually non-pathogenic) strain as shown in Table 2, were obtained from Dr. John Roth (University of Utah) and Dr. Tom Cebula (The Food and Drug Administration), respectively; these alleles (and additional alleles below) were transduced into virulent strain, 14028, constructing strains **2** and **5**, respectively. *DamΔ232* (strain **3**) was constructed using

internal oligonucleotides that serve as PCR primers designed to construct an in-frame 300 bp deletion of defined *Dam* sequence. *dcm1*::Km was constructed according to (Julio, S. M., *et al.*, *Molec. Gen. Genet.*, **258**: 178-181 (1998)); the Km resistance determinant is associated with an internal deletion of > 600 bp of *dcm* sequence. The *lrp31*::Km is a null insertion in the *lrp* gene (strain **6**). The Dam overproducing strain (strain **4**) contains *E. coli Dam* on a recombinant plasmid (pTP166) in a wild-type background (Marinus, *et al.*, *Gene*, **28**:123-125 (1984).

Please replace TABLE 1 on page 70 with the following TABLE 1:

TABLE 1

Strain	Genotype	Oral LD_{50}	I.P. LD_{50}	Competitive Index (I.P.)
1	"wild type"	$>10^{+5}$	<10	---
2	*Dam102::Mud-Cm*	$>10^{+9}$	$>10^{+4}$	$<10^{-4}$
3	*DamΔ232* (non-polar deletion)	$>10^{+9}$	$>10^{+4}$	$<10^{-4}$
4	wild type, (pTP166) (Dam overproducer)	10^{+8}	$>10^{+4}$	$<10^{-4}$
5	*mutS121::Tn10*	10^{+5}	ND	0.9
6	*lrp31::Km*	10^{+5}	ND	10.0
7	LT2	ND	$2 \times 10^{+4}$	ND

In the Claims:

Please cancel claim 5, add new claims 30 and 31 and amend claims 1, 3, 4, 7, and 18 to read as below:

1. (Amended) An immunogenic composition, comprising:

a pharmaceutically acceptable excipient; and